

0570
0731

ENTERED

see p. 6



OIIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/027,629

DATE: 08/08/2002

TIME: 10:39:16

Input Set : A:\07334-341001.TXT

Output Set : N:\CRF3\08082002\J027629.raw

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4 <110> APPLICANT: Bertin, John
5   Manji, Gulam A.
7 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN DOMAIN
8   PROTEIN FAMILY AND USES THEREOF
10 <130> FILE REFERENCE: 07334-341001
12 <140> CURRENT APPLICATION NUMBER: US 10/027,629
13 <141> CURRENT FILING DATE: 2001-12-20
15 <150> PRIOR APPLICATION NUMBER: US 09/964,955
16 <151> PRIOR FILING DATE: 2001-09-26
18 <150> PRIOR APPLICATION NUMBER: US 09/653,901
19 <151> PRIOR FILING DATE: 2000-09-01
21 <150> PRIOR APPLICATION NUMBER: US 09/506,067
22 <151> PRIOR FILING DATE: 2000-02-17
24 <160> NUMBER OF SEQ ID NOS: 17
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 3431
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (78)...(3176)
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40           Met Gly Phe Asn Leu Gln Ala Leu Leu Gln
41           1           5           10
43 ctc agc cag gat gag ttg agc aag ttc aag tat ctg atc acg acc ttc      158
44 Leu Ser Gln Asp Glu Leu Ser Lys Phe Lys Tyr Leu Ile Thr Thr Phe
45           15           20           25
47 tcc ccg gca cac gag ctc cag aag atc ccc cac aag gag gta gac aag      206
48 Ser Pro Ala His Glu Leu Gln Lys Ile Pro His Lys Glu Val Asp Lys
49           30           35           40
51 gct gat ggg aag caa ctg gta gaa atc ctc acc acc cat tgt gac agc      254
52 Ala Asp Gly Lys Gln Leu Val Glu Ile Leu Thr Thr His Cys Asp Ser
53           45           50           55
55 tac tgg gtg gag atg gcg agc ctc cag gtc ttt gaa aag atg cac cga      302
56 Tyr Trp Val Glu Met Ala Ser Leu Gln Val Phe Glu Lys Met His Arg
57 60           65           70           75
59 atg gat ctg tct gag aga gca aag gat gaa gtc aga gaa gca gct ttg      350
60 Met Asp Leu Ser Glu Arg Ala Lys Asp Glu Val Arg Glu Ala Ala Leu
61           80           85           90
63 aaa tcc ttt aat aaa agg aag cct cta tca tta ggg ata aca cgg aaa      398

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64	Lys	Ser	Phe	Asn	Lys	Arg	Lys	Pro	Leu	Ser	Leu	Gly	Ile	Thr	Arg	Lys	
65				95					100					105			
67	gaa	cga	cca	cct	cta	gac	gtg	gac	gaa	atg	ctg	gag	cgc	ttc	aaa	aca	446
68	Glu	Arg	Pro	Pro	Leu	Asp	Val	Asp	Glu	Met	Leu	Glu	Arg	Phe	Lys	Thr	
69			110					115					120				
71	gaa	gca	caa	gac	aaa	gac	aat	agg	tgc	agg	tat	ata	ttg	aag	acg	aag	494
72	Glu	Ala	Gln	Asp	Lys	Asp	Asn	Arg	Cys	Arg	Tyr	Ile	Leu	Lys	Thr	Lys	
73		125						130					135				
75	ttc	cgg	gag	atg	tgg	aag	agc	tgg	cct	gga	gat	agc	aaa	gag	gtc	cag	542
76	Phe	Arg	Glu	Met	Trp	Lys	Ser	Trp	Pro	Gly	Asp	Ser	Lys	Glu	Val	Gln	
77	140					145					150					155	
79	gtt	atg	gct	gag	aga	tac	aag	atg	ctg	atc	cca	ttt	agc	aac	ccc	agg	590
80	Val	Met	Ala	Glu	Arg	Tyr	Lys	Met	Leu	Ile	Pro	Phe	Ser	Asn	Pro	Arg	
81					160					165					170		
83	gtg	ctt	ccc	ggg	ccc	ttc	tca	tac	acg	gtg	gtg	ctg	tat	ggt	cct	gca	638
84	Val	Leu	Pro	Gly	Pro	Phe	Ser	Tyr	Thr	Val	Val	Leu	Tyr	Gly	Pro	Ala	
85				175					180					185			
87	ggc	ctt	ggg	aaa	acc	acg	ctg	gcc	cag	aaa	cta	atg	cta	gac	tgg	gca	686
88	Gly	Leu	Gly	Lys	Thr	Thr	Leu	Ala	Gln	Lys	Leu	Met	Leu	Asp	Trp	Ala	
89			190					195					200				
91	gag	gac	aac	ctc	atc	cac	aaa	ttc	aaa	tat	gcg	ttc	tac	ctc	agc	tgc	734
92	Glu	Asp	Asn	Leu	Ile	His	Lys	Phe	Lys	Tyr	Ala	Phe	Tyr	Leu	Ser	Cys	
93		205					210					215					
95	agg	gag	ctc	agc	cgc	ctg	ggc	ccg	tgc	agt	ttt	gca	gag	ctg	gtc	ttc	782
96	Arg	Glu	Leu	Ser	Arg	Leu	Gly	Pro	Cys	Ser	Phe	Ala	Glu	Leu	Val	Phe	
97	220				225					230					235		
99	agg	gac	tgg	cct	gaa	ttg	cag	gat	gac	att	cca	cac	atc	cta	gcc	caa	830
100	Arg	Asp	Trp	Pro	Glu	Leu	Gln	Asp	Asp	Ile	Pro	His	Ile	Leu	Ala	Gln	
101				240						245					250		
103	gca	cgg	aaa	atc	ttg	ttc	gtg	att	gac	ggc	ttt	gat	gag	ctg	gga	gcc	878
104	Ala	Arg	Lys	Ile	Leu	Phe	Val	Ile	Asp	Gly	Phe	Asp	Glu	Leu	Gly	Ala	
105			255						260					265			
107	gca	cct	ggg	gcg	ctg	atc	gag	gac	atc	tgc	ggg	gac	tgg	gag	aag	aag	926
108	Ala	Pro	Gly	Ala	Leu	Ile	Glu	Asp	Ile	Cys	Gly	Asp	Trp	Glu	Lys	Lys	
109			270					275					280				
111	aag	ccg	gtg	ccc	gtc	ctc	ctg	ggg	agt	ttg	ctg	aac	agg	gtg	atg	tta	974
112	Lys	Pro	Val	Pro	Val	Leu	Leu	Gly	Ser	Leu	Leu	Asn	Arg	Val	Met	Leu	
113		285					290					295					
115	ccc	aag	gcc	gcc	ctg	ctg	gtc	acc	acg	cgg	ccc	agg	gcc	ctg	agg	gac	1022
116	Pro	Lys	Ala	Ala	Leu	Leu	Val	Thr	Thr	Arg	Pro	Arg	Ala	Leu	Arg	Asp	
117	300					305					310				315		
119	ctc	cgg	atc	ctg	gcg	gag	gag	ccg	atc	tac	ata	agg	gtg	gag	ggc	ttc	1070
120	Leu	Arg	Ile	Leu	Ala	Glu	Glu	Pro	Ile	Tyr	Ile	Arg	Val	Glu	Gly	Phe	
121				320						325				330			
123	ctg	gag	gag	gac	aag	agg	gcc	tat	ttc	ctg	aga	cac	ttt	gga	gac	gag	1118
124	Leu	Glu	Glu	Asp	Lys	Arg	Ala	Tyr	Phe	Leu	Arg	His	Phe	Gly	Asp	Glu	
125				335					340					345			
127	gac	caa	gcc	atg	cgt	gcc	ttt	gag	cta	atg	agg	agc	aac	gcg	gcc	ctg	1166
128	Asp	Gln	Ala	Met	Arg	Ala	Phe	Glu	Leu	Met	Arg	Ser	Asn	Ala	Ala	Leu	

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131	ttc cag ctg ggc tgc gcc ccc gcg gtg tgc tgg atc gtg tgc acg act	1214		
132	Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile Val Cys Thr Thr			
133	365 370 375			
135	ctg aag ctg cag atg gag aag ggg gag gac ccg gtc ccc acc tgc ctc	1262		
136	Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Val Pro Thr Cys Leu			
137	380 385 390 395			
139	acc cgc acg ggg ctg ttc ctg cgt ttc ctc tgc agc ccg ttc ccg cag	1310		
140	Thr Arg Thr Gly Leu Phe Leu Arg Phe Leu Cys Ser Arg Phe Pro Gln			
141	400 405 410			
143	ggc gca cag ctg ccg ggc gcg ctg ccg acg ctg agc ctc ctg gcc gcg	1358		
144	Gly Ala Gln Leu Arg Gly Ala Leu Arg Thr Leu Ser Leu Leu Ala Ala			
145	415 420 425			
147	cag ggc ctg tgg gcg cag acg tcc gtg ctt cac cga gag gat ctg gaa	1406		
148	Gln Gly Leu Trp Ala Gln Thr Ser Val Leu His Arg Glu Asp Leu Glu			
149	430 435 440			
151	agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg gac gga gac	1454		
152	Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu Asp Gly Asp			
153	445 450 455			
155	atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac tcc ttc atc cac	1502		
156	Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser Phe Ile His			
157	460 465 470 475			
159	ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac acc ctg gag aag	1550		
160	Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Thr Leu Glu Lys			
161	480 485 490			
163	gag gag gaa gag gat agg gac ggc cac acc tgg gac att ggg gac gta	1598		
164	Glu Glu Glu Glu Asp Arg Asp Gly His Thr Trp Asp Ile Gly Asp Val			
165	495 500 505			
167	cag aag ctg ctt tcc gga gta gaa aga ctc agg aac ccc gac ctg atc	1646		
168	Gln Lys Leu Leu Ser Gly Val Glu Arg Leu Arg Asn Pro Asp Leu Ile			
169	510 515 520			
171	caa gca ggc tac tac tcc ttt ggc ctc gct aac gag aag aga gcc aag	1694		
172	Gln Ala Gly Tyr Tyr Ser Phe Gly Leu Ala Asn Glu Lys Arg Ala Lys			
173	525 530 535			
175	gag ttg gag gcc act ttt ggc tgc ccg atg tca ccg gac atc aaa cag	1742		
176	Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp Ile Lys Gln			
177	540 545 550 555			
179	gaa ttg ctg cga tgc gac ata agt tgt aag ggt gga cat tca acg gtg	1790		
180	Glu Leu Leu Arg Cys Asp Ile Ser Cys Lys Gly Gly His Ser Thr Val			
181	560 565 570			
183	aca gac ctg cag gag ctc ctc ggc tgt ctg tac gag tct cag gag gag	1838		
184	Thr Asp Leu Gln Glu Leu Leu Gly Cys Leu Tyr Glu Ser Gln Glu Glu			
185	575 580 585			
187	gag ctg gtg aag gag gtg atg gct cag ttc aaa gaa ata tcc ctg cac	1886		
188	Glu Leu Val Lys Glu Val Met Ala Gln Phe Lys Glu Ile Ser Leu His			
189	590 595 600			
191	tta aat gca gta gac gtt gtg cca tct tca ttc tgc gtc aag cac tgt	1934		
192	Leu Asn Ala Val Asp Val Val Pro Ser Ser Phe Cys Val Lys His Cys			
193	605 610 615			

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195	cga	aac	ctg	cag	aaa	atg	tca	ctg	cag	gta	ata	aag	gag	aat	ctc	ccg	1982
196	Arg	Asn	Leu	Gln	Lys	Met	Ser	Leu	Gln	Val	Ile	Lys	Glu	Asn	Leu	Pro	
197	620				625					630						635	
199	gag	aat	gtc	act	gcg	tct	gaa	tca	gac	gcc	gag	gtt	gag	aga	tcc	cag	2030
200	Glu	Asn	Val	Thr	Ala	Ser	Glu	Ser	Asp	Ala	Glu	Val	Glu	Arg	Ser	Gln	
201				640					645						650		
203	gat	gat	cag	cac	atg	ctt	cct	ttc	tgg	acg	gac	ctt	tgt	tcc	ata	ttt	2078
204	Asp	Asp	Gln	His	Met	Leu	Pro	Phe	Trp	Thr	Asp	Leu	Cys	Ser	Ile	Phe	
205				655					660					665			
207	gga	tca	aat	aag	gat	ctg	atg	ggt	cta	gca	atc	aat	gat	agc	ttt	ctc	2126
208	Gly	Ser	Asn	Lys	Asp	Leu	Met	Gly	Leu	Ala	Ile	Asn	Asp	Ser	Phe	Leu	
209			670					675					680				
211	agt	gcc	tcc	cta	gta	agg	atc	ctg	tgt	gaa	caa	ata	gcc	tct	gac	acc	2174
212	Ser	Ala	Ser	Leu	Val	Arg	Ile	Leu	Cys	Glu	Gln	Ile	Ala	Ser	Asp	Thr	
213		685				690					695						
215	tgt	cat	ctc	cag	aga	gtg	gtg	ttc	aaa	aac	att	tcc	cca	gct	gat	gct	2222
216	Cys	His	Leu	Gln	Arg	Val	Val	Phe	Lys	Asn	Ile	Ser	Pro	Ala	Asp	Ala	
217	700				705				710						715		
219	cat	cgg	aac	ctc	tgc	cta	gct	ctt	cga	ggt	cac	aag	act	gta	acg	tat	2270
220	His	Arg	Asn	Leu	Cys	Leu	Ala	Leu	Arg	Gly	His	Lys	Thr	Val	Thr	Tyr	
221				720					725					730			
223	ctg	acc	ctt	caa	ggc	aat	gac	cag	gat	gat	atg	ttt	ccc	gca	ttg	tgt	2318
224	Leu	Thr	Leu	Gln	Gly	Asn	Asp	Gln	Asp	Asp	Met	Phe	Pro	Ala	Leu	Cys	
225			735					740					745				
227	gag	gtc	ttg	aga	cat	cca	gaa	tgt	aac	ctg	cga	tat	ctc	ggg	ttg	gtg	2366
228	Glu	Val	Leu	Arg	His	Pro	Glu	Cys	Asn	Leu	Arg	Tyr	Leu	Gly	Leu	Val	
229		750					755					760					
231	tct	tgt	tcc	gct	acc	act	cag	cag	tgg	gct	gat	ctc	tcc	ttg	gcc	ctt	2414
232	Ser	Cys	Ser	Ala	Thr	Thr	Gln	Gln	Trp	Ala	Asp	Leu	Ser	Leu	Ala	Leu	
233		765				770					775						
235	gaa	gtc	aac	cag	tcc	ctg	acg	tgc	gta	aac	ctc	tcc	gac	aat	gag	ctt	2462
236	Glu	Val	Asn	Gln	Ser	Leu	Thr	Cys	Val	Asn	Leu	Ser	Asp	Asn	Glu	Leu	
237	780				785				790						795		
239	ctg	gat	gag	ggt	gct	aag	ttg	ctg	tac	aca	act	ttg	aga	cac	ccc	aag	2510
240	Leu	Asp	Glu	Gly	Ala	Lys	Leu	Leu	Tyr	Thr	Leu	Arg	His	Pro	Lys		
241				800					805					810			
243	tgc	ttt	ctg	cag	agg	ttg	tgc	ttg	gaa	aac	tgt	cac	ctt	aca	gaa	gcc	2558
244	Cys	Phe	Leu	Gln	Arg	Leu	Ser	Leu	Glu	Asn	Cys	His	Leu	Thr	Glu	Ala	
245			815					820					825				
247	aat	tgc	aag	gac	ctt	gct	gct	gtg	ttg	gtt	gtc	agc	cgg	gag	ctg	aca	2606
248	Asn	Cys	Lys	Asp	Leu	Ala	Ala	Val	Leu	Val	Val	Ser	Arg	Glu	Leu	Thr	
249		830				835					840						
251	cac	ctg	tgc	ttg	gcc	aag	aac	ccc	att	ggg	aat	aca	ggg	gtg	aag	ttt	2654
252	His	Leu	Cys	Leu	Ala	Lys	Asn	Pro	Ile	Gly	Asn	Thr	Gly	Val	Lys	Phe	
253		845				850					855						
255	ctg	tgt	gag	ggc	ttg	agg	tac	ccc	gag	tgt	aaa	ctg	cag	acc	ttg	gtg	2702
256	Leu	Cys	Glu	Gly	Leu	Arg	Tyr	Pro	Glu	Cys	Lys	Leu	Gln	Thr	Leu	Val	
257	860				865				870						875		
259	ctt	tgg	aac	tgc	gac	ata	act	agc	gat	ggc	tgc	tgc	gat	ctc	aca	aag	2750

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263 ctt ctc caa gaa aaa tca agc ctg ttg tgt ttg gat ctg ggg ctg aat      2798
264 Leu Leu Gln Glu Lys Ser Ser Leu Leu Cys Leu Asp Leu Gly Leu Asn
265      895      900      905
267 cac ata gga gtt aag gga atg aag ttc ctg tgt gag gct ttg agg aaa      2846
268 His Ile Gly Val Lys Gly Met Lys Phe Leu Cys Glu Ala Leu Arg Lys
269      910      915      920
271 cca ctg tgc aac ttg aga tgt ctg tgg ttg tgg gga tgt tcc atc cct      2894
272 Pro Leu Cys Asn Leu Arg Cys Leu Trp Leu Trp Gly Cys Ser Ile Pro
273      925      930      935
275 ccg ttc agt tgt gaa gac ctc tgc tct gcc ctc agc aac cag agc ctc      2942
276 Pro Phe Ser Cys Glu Asp Leu Cys Ser Ala Leu Ser Asn Gln Ser Leu
277 940      945      950      955
279 gtc act ctg gac ctg ggt cag aat ccc ttg ggg tct agt gga gtg aag      2990
280 Val Thr Leu Asp Leu Gly Gln Asn Pro Leu Gly Ser Ser Gly Val Lys
281      960      965      970
283 atg ctg ttt gaa acc ttg aca tgt tcc agt ggc acc ctc cgg aca ctc      3038
284 Met Leu Phe Glu Thr Leu Thr Cys Ser Ser Gly Thr Leu Arg Thr Leu
285      975      980      985
287 agg ttg aaa atc gat gac ttt aat gat gaa ctc aat aag ctg ctg gaa      3086
288 Arg Leu Lys Ile Asp Asp Phe Asn Asp Glu Leu Asn Lys Leu Leu Glu
289      990      995      1000
291 gaa ata gaa gaa aaa aac cca caa ctg att att gat act gag aaa cat      3134
292 Glu Ile Glu Glu Lys Asn Pro Gln Leu Ile Ile Asp Thr Glu Lys His
293      1005      1010      1015
295 cat ccc tgg gca gaa agg cct tct tct cat gac ttc atg atc      3176
296 His Pro Trp Ala Glu Arg Pro Ser Ser His Asp Phe Met Ile
297 1020      1025      1030
299 tgaatcccc cgagtcattc attctccatg aagtcacga ttttccaggt gttggtgaac      3236
300 tgccgtgtgac tctctctc cccggccct acccctcagg gataatgagt tcattgctgg      3296
301 gctagatgtt ttagccatga ttctgctct gttttatacc tgcacacatc cttatctttg      3356
302 ttacatatga aatatctgta tcacgggtat attgagagaa ataaaggtga gagcattcac      3416
303 aaaaaaaaaa aaaaa      3431
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313 Leu Ser Lys Phe Lys Tyr Leu Ile Thr Thr Phe Ser Pro Ala His Glu
314      20      25      30
315 Leu Gln Lys Ile Pro His Lys Glu Val Asp Lys Ala Asp Gly Lys Gln
316      35      40      45
317 Leu Val Glu Ile Leu Thr Thr His Cys Asp Ser Tyr Trp Val Glu Met
318      50      55      60
319 Ala Ser Leu Gln Val Phe Glu Lys Met His Arg Met Asp Leu Ser Glu
320 65      70      75      80

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 2,5,6,9,11,12,23,25,27,28,29,31,37,39,40,45,46,49,50,54

Seq#:10; Xaa Pos. 58,70,75

Seq#:11; Xaa Pos. 2,5,9,11,12,23,25,31,39

VERIFICATION SUMMARY

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L:1040 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1044 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:1045 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16
L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32
L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48
L:1053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:64
L:1064 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1068 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:1069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:1073 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:32